



SEQUENCE LISTING

<110> University of Victoria Innovation and Developement Corporation
Hintz, William E.
Eades, Caleb Joshua

<120> Mannosidases and Methods for using the Same

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<170> PatentIn version 3.3

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| actctgacgg gcatcggccc tgagcaattt agctgggacc ctaacgggttgc gcccggcagc | 1140 |
| cagaaggagc tgttcgagcg cgcaggcttc tacatcaaca gcggccaata cattttcggt | 1200 |
| cccgaaatca tcgagagctt ctactatgca tggcgctca caggtgtatgg aacgtaccc | 1260 |
| gaatgggtgt ggaacgcctt caccaacatc aacaagtact gccgcactgc gaccggtttc | 1320 |
| gcggggctgg agaacgtcaa tgcagcgaac ggccggaggcc ggatcgacaa ccaggagagt | 1380 |
| ttcatgttcg cagagggtgtt gaagtattcg tttttgactt ttgcttcgttgc ggacgactgg | 1440 |
| caggtgcaga agggcagtgg aaatacgttt gtttataaca ccgaggcgca cccgtttaag | 1500 |
| gtgtatacgc ctcag | 1515 |

<210> 6
 <211> 505
 <212> PRT
 <213> *Aspergillus nidulans*

<400> 6

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Arg | Thr | Lle | Lle | Ala | Lle | Ala | Ala | Phe | Ala | Gly | Phe | Ala | Ala | Ala | |
| 1 | | | | | 5 | | | | 10 | | | | 15 | | | |

Arg Val Pro Ala Thr Ala Ile Thr Arg Pro Val Met Arg Ser Asp Ser
20 25 30

Arg Ala Asp Ala Val Lys Glu Ala Phe Ser His Ala Trp Asp Gly Thr
35 40 45

Thr Asn Thr Ala Phe Pro His Asp Glu Leu His Pro Ile Ser Asn Gly
50 55 60

Thr Gly Asp Ser Arg Asn His Trp Gly Ala Ser Ala Val Asp Ala Leu
65 70 75 80

Ser Thr Ala Ile Met Met Arg Asn Ala Thr Ile Val Asn Gln Ile Leu
85 90 95

Asp His Ile Ala Ala Val Asp Thr Ser Lys Thr Asn Ala Met Val Ser
100 105 110

Leu Phe Glu Thr Thr Ile Arg Thr Leu Ala Gly Met Ile Ser Gly Thr
115 120 125

Asp Leu Leu Lys Gly Pro Ala Ala Gly Leu Val Asp Asp Ser Arg Val
130 135 140

Asp Val Leu Leu Glu Gln Ser Gln Asn Leu Ala Glu Val Leu Lys Phe
145 150 155 160

Ala Phe Asp Thr Pro Ser Gly Val Pro Thr Asn Met Ile Asn Ile Thr
165 170 175

Ser Gly Gly Asn Asp Gly Ala Thr Thr Asn Gly Leu Ala Val Thr Gly
180 185 190

Thr Leu Val Leu Glu Trp Thr Arg Leu Ser Asp Leu Thr Gly Asn Asp
195 200 205

Glu Thr Ala Arg Leu Ser Gln Arg Ala Glu Asp Thr Leu Leu His Pro
210 215 220

Glu Pro Ala Gln Thr Glu Pro Phe Pro Gly Leu Ile Gly Ser Ala Val
225 230 235 240

Asn Ile Ala Asp Gly Lys Leu Ala Asn Gly His Ile Ser Trp Asn Gly
245 250 255

Gly Ala Asp Ser Thr Thr Glu Thr Leu Ile Lys Met Thr Val Thr Asp
260 265 270

Pro Glu Arg Phe Gly Leu Thr Arg Asp Arg Trp Val Ala Ala Ala Glu
275 280 285

Ser Ser Ile Asn His Leu Ala Ser His Pro Ser Thr Arg Pro Asp Val
290 295 300

Thr Phe Leu Ala Thr Thr Asn Glu Glu His Gln Leu Gly Leu Thr Ser
305 310 315 320

Gln His Leu Thr Cys Phe Asp Gly Gly Ser Phe Leu Leu Gly Gly Thr
325 330 335

Leu Leu Asp Arg Gln Asp Phe Val Asp Phe Gly Leu Asp Leu Val Ala
340 345 350

Gly Cys His Glu Thr Thr Asn Ser Thr Leu Thr Gly Ile Gly Pro Glu
355 360 365

Gln Phe Ser Trp Asp Pro Asn Gly Val Pro Asp Ser Gln Lys Glu Leu
370 375 380

Phe Glu Arg Ala Gly Phe Thr Ile Asn Ser Gly Gln Thr Ile Leu Arg
385 390 395 400

Pro Glu Val Ile Glu Ser Phe Thr Thr Ala Trp Arg Val Thr Gly Asp
405 410 415

Gly Thr Thr Leu Glu Trp Val Trp Asn Ala Phe Thr Asn Ile Asn Lys
420 425 430

Thr Cys Arg Thr Ala Thr Gly Phe Ala Gly Leu Glu Asn Val Asn Ala
435 440 445

Ala Asn Gly Gly Arg Ile Asp Asn Gln Glu Ser Phe Met Phe Ala
450 455 460

Glu Val Leu Lys Thr Ser Phe Leu Thr Phe Ala Pro Glu Asp Asp Trp
465 470 475 480

Gln Val Gln Lys Gly Ser Gly Asn Thr Phe Val Thr Asn Thr Glu Ala
485 490 495

His Pro Phe Lys Val Thr Thr Pro Gln
500 505

<210> 7
<211> 6
<212> DNA
<213> Aspergillus nidulans

<400> 7
gtaagt 6

<210> 8
<211> 6
<212> DNA
<213> Aspergillus nidulans

<220>
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<222> (4)..(4)
<223> n is a, c, g, or t/u

<400> 8
gtangt 6

<210> 9
<211> 6
<212> DNA
<213> Aspergillus nidulans

<400> 9
gctgac 6

<210> 10
<211> 6
<212> DNA
<213> Aspergillus nidulans

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<222> (1)..(1)
<223> r is g or a

<220>
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<222> (4)..(4)
<223> r is g or a

<400> 10
rctrac 6

<210> 11
<211> 6
<212> DNA

<213> Aspergillus nidulans

<400> 11
gtacgt

6

<210> 12
<211> 6
<212> DNA
<213> Aspergillus nidulans

<400> 12
actgac

6

<210> 13
<211> 10
<212> PRT
<213> Aspergillus nidulans

<400> 13

Gly Gly Leu Gly Glu Ser Phe Thr Glu Thr
1 5 10

<210> 14
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<212> PRT
<213> Aspergillus nidulans

<400> 14

Leu Ala Glu Thr Leu Lys Thr Leu Thr
1 5

<210> 15
<211> 29
<212> DNA
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<220>
<223> PCR Primer

<220>
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<222> (3)..(3)
<223> y is t/u or c

<220>
<221> misc_feature
<222> (6)..(6)
<223> y is t/u or c

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g, or t/u

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<220>
<221> misc_feature
<222> (12)..(12)
<223> y is t/u or c

<220>
<221> misc_feature
<222> (15)..(15)
<223> r is g or a

<220>
<221> misc_feature
<222> (18)..(18)
<223> n is a, c, g, or t/u

<400> 15
gggggyctng gygارتcntt ctacgagta
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29

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<210> 16
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer
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<222> (4)..(4)
<223> n is a, c, g, or t/u

<220>
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<222> (13)..(13)
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<220>
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<222> (16)..(16)
<223> n is a, c, g, or t/u

<220>
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<222> (22)..(22)
<223> n is a, c, g, or t/u
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<220>
<221> misc_feature
<222> (25)..(25)
<223> n is a, c, g, or t/u

<220>
<221> misc_feature
<222> (28)..(28)
<223> r is g or a
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<220>
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<221> misc_feature
<222> (29)..(29)
<223> h is a, c, or t/u

<400> 16
gtanaggtac tttnaggtct cngcnagrha gaa

33

<210> 17
<211> 2032
<212> DNA
<213> Aspergillus nidulans

<220>
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<222> (36)..(1793)

<400> 17
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Met Pro Arg Arg Trp Ser
1 5

tcc ctc atc agc atc aca gcc atc ttc ttg gtc ctc ttc ttc ctc ctt 101
Ser Leu Ile Ser Ile Thr Ala Ile Phe Leu Val Leu Phe Phe Leu Leu
10 15 20

cat agg aat aca gac aca cca cgc gcc gca aat agg gct aca aac ggc 149
His Arg Asn Thr Asp Thr Pro Arg Ala Ala Asn Arg Ala Thr Asn Gly
25 30 35

cct gcc aac ggc ttt gct agg cag caa agc ata tgt cca tca aca ccc 197
Pro Ala Asn Gly Phe Ala Arg Gln Gln Ser Ile Cys Pro Ser Thr Pro
40 45 50

cct cag cct cca tat aac cga acc agc acg gga ggg ttc aac tgg ggt 245
Pro Gln Pro Pro Tyr Asn Arg Thr Ser Thr Gly Gly Phe Asn Trp Gly
55 60 65 70

gaa atc cca gtc aga tac cct gta tcc gac ttc atc ccg ctg tca acc 293
Glu Ile Pro Val Arg Tyr Pro Val Ser Asp Phe Ile Pro Leu Ser Thr
75 80 85

aac tct cct gca aca ctt ccg cgc atc caa cgc tct tcc ttc cca ctt 341
Asn Ser Pro Ala Thr Leu Pro Arg Ile Gln Arg Ser Ser Phe Pro Leu
90 95 100

caa tcc tca atc act aaa tcc cgc cag gca gca gtc aaa ggt gcc ttt 389
Gln Ser Ser Ile Thr Lys Ser Arg Gln Ala Ala Val Lys Gly Ala Phe
105 110 115

cag cgc gca tgg acc tcc tac aca acc cac gcc tgg aag gcg gac gag 437
Gln Arg Ala Trp Thr Ser Tyr Thr Thr His Ala Trp Lys Ala Asp Glu
120 125 130

gta cgg ccc atc acg gcc gga tct cga aac aac ttt ggc gga tgg gga 485
Val Arg Pro Ile Thr Ala Gly Ser Arg Asn Asn Phe Gly Gly Trp Gly
135 140 145 150

gcg acc cta gtc gac aat ctc gac aca ctg cta atc atg ggg ctg gac 533

| | | | | |
|--|-----|-----|-----|------|
| Ala Thr Leu Val Asp Asn Leu Asp Thr Leu Leu Ile Met Gly Leu Asp | 155 | 160 | 165 | |
| gag gag ttc gca gca gtc gac gca gtc gca gat ata gaa ttc agc Glu Glu Phe Ala Ala Val Asp Ala Leu Ala Asp Ile Glu Phe Ser | 170 | 175 | 180 | 581 |
| ccg cac tcg tcc cca tcc tcc cag agc aca atc aac ata ttc gaa Pro His Ser Ser Pro Ser Ser Gln Ser Thr Ile Asn Ile Phe Glu | 185 | 190 | 195 | 629 |
| acg aca atc cgg tat ctg ggc ggc ttg ctc gcg gcg tat gat ctc act Thr Thr Ile Arg Tyr Leu Gly Gly Leu Leu Ala Ala Tyr Asp Leu Thr | 200 | 205 | 210 | 677 |
| ggc tgt cga gag act cgg ctg ctg gac aaa gca atc cag ctt ggg gag Gly Cys Arg Glu Thr Arg Leu Leu Asp Lys Ala Ile Gln Leu Gly Glu | 215 | 220 | 225 | 725 |
| atg atc tac acc tcc ttc gac aca gag aac cgc atg ccc gta cca cgg Met Ile Tyr Thr Ser Phe Asp Thr Glu Asn Arg Met Pro Val Pro Arg | 235 | 240 | 245 | 773 |
| tgg aat ctg cac aaa gca ggc aac gga gag cct cag cgc gcg gca gtg Trp Asn Leu His Lys Ala Gly Asn Gly Glu Pro Gln Arg Ala Ala Val | 250 | 255 | 260 | 821 |
| cag ggc gtg ctc gct gaa ctc gcc agc agc agt ctc gag ttc acg cgg Gln Gly Val Leu Ala Glu Leu Ala Ser Ser Leu Glu Phe Thr Arg | 265 | 270 | 275 | 869 |
| ctg tcg cag ctg acg ggg gat atg cgg tat ttc gat gcg gca tcc cgc Leu Ser Gln Leu Thr Gly Asp Met Arg Tyr Phe Asp Ala Ala Ser Arg | 280 | 285 | 290 | 917 |
| att acc gat ctg ctt gac tcc caa gcc ggc cat acc cgg atc ccg ggg Ile Thr Asp Leu Leu Asp Ser Gln Ala Gly His Thr Arg Ile Pro Gly | 295 | 300 | 305 | 965 |
| ttg tgg cca gtc agc gtg aac ctg cag aaa ggc gat ctg acc cgt ggg Leu Trp Pro Val Ser Val Asn Leu Gln Lys Gly Asp Leu Thr Arg Gly | 315 | 320 | 325 | 1013 |
| tcg aca ttc agt ttt ggc ggg atg gcc gat agc gcc tac gag tat ctc Ser Thr Phe Ser Phe Gly Gly Met Ala Asp Ser Ala Tyr Glu Tyr Leu | 330 | 335 | 340 | 1061 |
| ggc aag acg tat cgg ctc ctc ggt ggt gtg ggg aaa ggg cca cag tac Gly Lys Thr Tyr Arg Leu Leu Gly Gly Val Gly Lys Gly Pro Gln Tyr | 345 | 350 | 355 | 1109 |
| gag cgt ctg gcg cga aac gca cta gat gcc ggg att cga cat ctc ctc Glu Arg Leu Ala Arg Asn Ala Leu Asp Ala Gly Ile Arg His Leu Leu | 360 | 365 | 370 | 1157 |
| ttc cga ccg atg acg cct gat cat gca gat atc ctc cta ccc ggg gtc Phe Arg Pro Met Thr Pro Asp His Ala Asp Ile Leu Leu Pro Gly Val | 375 | 380 | 385 | 1205 |
| gcg cac gca acc agc tct tcc gtg gga ctc gag ccc cgg aca gag cat | | | | 1253 |

| | | | |
|---|-----|------|-----|
| Ala His Ala Thr Ser Ser Ser Val Gly Leu Glu Pro Arg Thr Glu His | | | |
| 395 | 400 | 405 | |
| ctc gcc tgt ttt gtg ggt ggg atg tac gcg ctc gcc ggg aag ctt ttc | | 1301 | |
| Leu Ala Cys Phe Val Gly Gly Met Tyr Ala Leu Ala Gly Lys Leu Phe | | | |
| 410 | 415 | 420 | |
| tca aac cag acg tac ctc gac acc ggc cgg aag ctg aca gac ggt tgt | | 1349 | |
| Ser Asn Gln Thr Tyr Leu Asp Thr Gly Arg Lys Leu Thr Asp Gly Cys | | | |
| 425 | 430 | 435 | |
| atc tgg tac tac gat aat tca ccg cta ggt atc atg ccg gag atg ttc | | 1397 | |
| Ile Trp Tyr Tyr Asp Asn Ser Pro Leu Gly Ile Met Pro Glu Met Phe | | | |
| 440 | 445 | 450 | |
| acc gtg ccg gct tgt ccg tca gtg gct gaa tgt cct tgg gac gaa aca | | 1445 | |
| Thr Val Pro Ala Cys Pro Ser Val Ala Glu Cys Pro Trp Asp Glu Thr | | | |
| 455 | 460 | 465 | 470 |
| agg ggt ggt atc tac acc tac gtg cgt gat ggg cac tac ttt ctg cgt | | 1493 | |
| Arg Gly Gly Ile Tyr Thr Tyr Val Arg Asp Gly His Tyr Phe Leu Arg | | | |
| 475 | 480 | 485 | |
| cct gag gca atg gag agt atc ttc tat atg tgg cgc att aca ggg gac | | 1541 | |
| Pro Glu Ala Met Glu Ser Ile Phe Tyr Met Trp Arg Ile Thr Gly Asp | | | |
| 490 | 495 | 500 | |
| gaa aag tac cgc gag gct gca tgg aga atg ttc acg gct atc gaa gcg | | 1589 | |
| Glu Lys Tyr Arg Glu Ala Ala Trp Arg Met Phe Thr Ala Ile Glu Ala | | | |
| 505 | 510 | 515 | |
| gtt aca aag acg gag ttt ggg aat gcg gcg gtg cgg gat gtt atg gtt | | 1637 | |
| Val Thr Lys Thr Glu Phe Gly Asn Ala Ala Val Arg Asp Val Met Val | | | |
| 520 | 525 | 530 | |
| gag gaa gga aat gta aag aga gaa gat agc atg gag agt ttc tgg atg | | 1685 | |
| Glu Glu Gly Asn Val Lys Arg Glu Asp Ser Met Glu Ser Phe Trp Met | | | |
| 535 | 540 | 545 | 550 |
| gca gag acg ttg aag tat ctg tat ctg ata ttt ggg gag acc gat ttg | | 1733 | |
| Ala Glu Thr Leu Lys Tyr Leu Tyr Leu Ile Phe Gly Glu Thr Asp Leu | | | |
| 555 | 560 | 565 | |
| gtc agc ttg gac tgg gtg ttc aat acg gag gcg cac cct ttg agg | | 1781 | |
| Val Ser Leu Asp Asp Trp Val Phe Asn Thr Glu Ala His Pro Leu Arg | | | |
| 570 | 575 | 580 | |
| ggt gca ggg agt tgacattgta ttcacacatc ggtatagaca aattatagag | | 1833 | |
| Gly Ala Gly Ser | | | |
| 585 | | | |
| tagacgttca aaacggccaa aactgaatgg atagactcca tatgcattga atatacaatg | | 1893 | |
| tattcgctgc aaagcatgga taaaataaag atgtacaaag tgtctttgtt gtcgctttga | | 1953 | |
| aagtggata tcatccatc ataagggtggc agtgtaaacca accctctata tcacccat | | 2013 | |
| agacagctga tagaccggc | | 2032 | |

<210> 18
<211> 586
<212> PRT
<213> Aspergillus nidulans

<400> 18

Met Pro Arg Arg Trp Ser Ser Leu Ile Ser Ile Thr Ala Ile Phe Leu
1 5 10 15

Val Leu Phe Phe Leu Leu His Arg Asn Thr Asp Thr Pro Arg Ala Ala
20 25 30

Asn Arg Ala Thr Asn Gly Pro Ala Asn Gly Phe Ala Arg Gln Gln Ser
35 40 45

Ile Cys Pro Ser Thr Pro Pro Gln Pro Pro Tyr Asn Arg Thr Ser Thr
50 55 60

Gly Gly Phe Asn Trp Gly Glu Ile Pro Val Arg Tyr Pro Val Ser Asp
65 70 75 80

Phe Ile Pro Leu Ser Thr Asn Ser Pro Ala Thr Leu Pro Arg Ile Gln
85 90 95

Arg Ser Ser Phe Pro Leu Gln Ser Ser Ile Thr Lys Ser Arg Gln Ala
100 105 110

Ala Val Lys Gly Ala Phe Gln Arg Ala Trp Thr Ser Tyr Thr Thr His
115 120 125

Ala Trp Lys Ala Asp Glu Val Arg Pro Ile Thr Ala Gly Ser Arg Asn
130 135 140

Asn Phe Gly Gly Trp Gly Ala Thr Leu Val Asp Asn Leu Asp Thr Leu
145 150 155 160

Leu Ile Met Gly Leu Asp Glu Glu Phe Ala Ala Ala Val Asp Ala Leu
165 170 175

Ala Asp Ile Glu Phe Ser Pro His Ser Ser Pro Ser Ser Gln Ser
180 185 190

Thr Ile Asn Ile Phe Glu Thr Thr Ile Arg Tyr Leu Gly Gly Leu Leu
195 200 205

Ala Ala Tyr Asp Leu Thr Gly Cys Arg Glu Thr Arg Leu Leu Asp Lys

210

215

220

Ala Ile Gln Leu Gly Glu Met Ile Tyr Thr Ser Phe Asp Thr Glu Asn
225 230 235 240

Arg Met Pro Val Pro Arg Trp Asn Leu His Lys Ala Gly Asn Gly Glu
245 250 255

Pro Gln Arg Ala Ala Val Gln Gly Val Leu Ala Glu Leu Ala Ser Ser
260 265 270

Ser Leu Glu Phe Thr Arg Leu Ser Gln Leu Thr Gly Asp Met Arg Tyr
275 280 285

Phe Asp Ala Ala Ser Arg Ile Thr Asp Leu Leu Asp Ser Gln Ala Gly
290 295 300

His Thr Arg Ile Pro Gly Leu Trp Pro Val Ser Val Asn Leu Gln Lys
305 310 315 320

Gly Asp Leu Thr Arg Gly Ser Thr Phe Ser Phe Gly Gly Met Ala Asp
325 330 335

Ser Ala Tyr Glu Tyr Leu Gly Lys Thr Tyr Arg Leu Leu Gly Val
340 345 350

Gly Lys Gly Pro Gln Tyr Glu Arg Leu Ala Arg Asn Ala Leu Asp Ala
355 360 365

Gly Ile Arg His Leu Leu Phe Arg Pro Met Thr Pro Asp His Ala Asp
370 375 380

Ile Leu Leu Pro Gly Val Ala His Ala Thr Ser Ser Val Gly Leu
385 390 395 400

Glu Pro Arg Thr Glu His Leu Ala Cys Phe Val Gly Gly Met Tyr Ala
405 410 415

Leu Ala Gly Lys Leu Phe Ser Asn Gln Thr Tyr Leu Asp Thr Gly Arg
420 425 430

Lys Leu Thr Asp Gly Cys Ile Trp Tyr Tyr Asp Asn Ser Pro Leu Gly
435 440 445

Ile Met Pro Glu Met Phe Thr Val Pro Ala Cys Pro Ser Val Ala Glu

450

455

460

Cys Pro Trp Asp Glu Thr Arg Gly Gly Ile Tyr Thr Tyr Val Arg Asp
465 470 475 480

Gly His Tyr Phe Leu Arg Pro Glu Ala Met Glu Ser Ile Phe Tyr Met
485 490 495

Trp Arg Ile Thr Gly Asp Glu Lys Tyr Arg Glu Ala Ala Trp Arg Met
500 505 510

Phe Thr Ala Ile Glu Ala Val Thr Lys Thr Glu Phe Gly Asn Ala Ala
515 520 525

Val Arg Asp Val Met Val Glu Glu Gly Asn Val Lys Arg Glu Asp Ser
530 535 540

Met Glu Ser Phe Trp Met Ala Glu Thr Leu Lys Tyr Leu Tyr Leu Ile
545 550 555 560

Phe Gly Glu Thr Asp Leu Val Ser Leu Asp Asp Trp Val Phe Asn Thr
565 570 575

Glu Ala His Pro Leu Arg Gly Ala Gly Ser
580 585

<210> 19
<211> 6
<212> DNA
<213> Artificial Sequence

<220>
<223> Consensus Splice Site

<220>
<221> misc_feature
<222> (1)..(1)
<223> r is g or a

<220>
<221> misc_feature
<222> (4)..(4)
<223> r is g or a

<400> 19
rctrac

6